UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/758,562	01/16/2004	Akira Saito	Q79447	5978

23373 7590 09/11/2006

SUGHRUE MION, PLLC
2100 PENNSYLVANIA AVENUE, N.W.
SUITE 800
WASHINGTON, DC 20037

EXAMINER	
JOYCE, CATHERINE	

ART UNIT	PAPER NUMBER
1642	

DATE MAILED: 09/11/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/758,562	SAITO ET AL.	
	Examiner	Art Unit	
	Catherine M. Joyce	1642	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *08 June 2006*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-5,7 and 9-21* is/are pending in the application.

4a) Of the above claim(s) *3, 4, 11-14, and 19-21* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☐ Claim(s) _____ is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date 8/24/05
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

1. Claims 1-5, 7, and 9-21 are pending, and claims 3, 4, 11-14, and 19-21 are withdrawn from consideration as being drawn to a non-elected invention

2. Claims 1, 2, 5, 7, 9-10, and 15-18 are under examination.

3. Applicant's election of the invention Group I, and the species 1 (SEQ ID NO:8 and SEQ ID NO:9, corresponding to claim 18), in the reply filed on June 8, 2006 is acknowledged. Because Applicant did not point out any errors in the restriction requirement, the election is treated as an election without traverse.

Claim Rejections - 35 USC § 112

4. The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

5. Claims 9 and 10 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claims contain subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The factors to be considered in determining whether undue experimentation is required are summarized In re Wands 858 F.2d 731, 8 USPQ2nd 1400 (Fed. Cir, 1988). The court in Wands states: "Enablement is not precluded by the necessity for some experimentation such as routine screening. However, experimentation needed to practice the invention must not be undue experimentation. The key word is 'undue,' not 'experimentation.' " (Wands, 8 USPQ2d 1404). Clearly, enablement of a claimed invention cannot be predicated on the basis of quantity of experimentation required to

make or use the invention. "Whether undue experimentation is needed is not a single, simple factual determination, but rather is a conclusion reached by weighing many factual considerations." (Wands, 8 USPQ2d 1404). The factors to be considered in determining whether undue experimentation is required include: (1) the quantity of experimentation necessary, (2) the amount or direction or guidance presented, (3) the presence or absence of working examples, (4) the nature of the invention, (5) the state of the prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the claims.

The claims are drawn to the following:

a process for producing a recombinant polypeptide or its salts comprising the amino acid sequence of SEQ ID NO:1 comprising the steps of:

transforming a host cell with a recombinant vector comprising a polynucleotide encoding the polypeptide represented by SEQ ID NO:1, thereby creating a transformed cell;

culturing the transformed cell whereby the transformed cell produces said polypeptide; and

collecting said recombinant polypeptide from the culture (claim 9);

a process for producing a recombinant oncogenic protein comprising an amino acid sequence of SEQ ID NO:1 comprising the steps of:

transforming a host cell with a recombinant vector comprising a polynucleotide encoding an oncogenic protein with the amino acid sequence of SEQ ID NO:1, thereby creating a transformed cell;

culturing the transformed cell whereby the transformed cell produces said recombinant oncogenic protein; and

collecting said recombinant polypeptide from the culture (claim 10);

The specification teaches the cloning and sequencing of a human cDNA encoding a hWAPL protein using a human testicular cDNA kit (Example 1). The

specification also teaches that among carcinoma cells examined of cervical cancer, corpus uteri cancer, ovarian cancer, gastric cancer, renal cancer, pulmonary cancer, colorectal cancer, and breast cancer, about 40% of carcinoma cell samples of cervical cancer demonstrated significant hWAPL gene expression and that some gastric cancers also demonstrated high expression of the hWAPL gene (Example 2). The specification also teaches that transfection of a human epidermal cell line (HDK1) to express the HPV E6 gene product resulted in cleavage of the p53 tumor suppressor protein and expression of the hWAPL gene (Example 3). The specification also teaches that when cell lines CaSki, SiHa and C33A were transfected with MSCV-puro BPV1E2, CaSki and SiHa cell lines producing E6 and E7 from HPV16 demonstrated increase of the remained p53 tumor suppressor protein as a result of inhibiting transcription of E6 and E7 genes by the E2 from HPV, with concomitant inhibition of expression of the hWAPL, whereas in the C33A cell line, in which cancerization is induced by mechanisms other than by HPV infection, remain levels of the p53 protein or expression levels of hWAPL protein were unaffected (Example 3). The specification also teaches that transforming a HeLa cells with a p53 expression vector reduced that amount of luciferase reporter protein that was producing using a hWAPL promoter attached to the luciferase gene (Example 4). The specification also teaches the construction of an expression vector for producing hWAPL fused to a green fluorescent protein and the transfection of a host mammalian cell with the vector with concomitant selection, wherein a transformed host cell line carrying the desired expression vector for expressing the hWAPL protein was obtained (Example 5). The specification also teaches that a HeLa cell infected with the an expression vector for the hWAPL-green fluorescent protein fusion is selected to select cells positive and negative for hWAPL protein expression, wherein cells that a negative of hWAPL protein expression show a chromosome gene content similar to that of the host HeLa cells whereas cells that are positive for hWAPL protein expression show an increase in the amount of polyploidy chromosomes and the induction of multi-nucleation (Example 7). The specification also teaches that NIH 3T3 cells that were transfected with an expression vector for hWAPL, with western blot confirmation of protein expression, form a focus structure in cell

culture whereas control cells form a single-cell confluent layer, and that the transfected cells that were injected into mice were oncogenic (Example 8). The specification also teaches that a small inhibitory RNA that was targeted to the hWAPL gene inhibited cell growth of SiHa cervical cancer cell line, that the SiHa cell lines formed tumors in mice, and that injection of the tumors with a siRNA resulted in a reduction in tumor size (Example 9).

The teaching of the specification cannot be reasonably extrapolated to enable the claims because the teaching in the specification (i) that the RNA encoding the hWAPL protein is expressed in human cancers and (ii) that transfection of a cell line with the hWAPL gene is not sufficient to establish that the hWAPL protein is oncogenic or is involved in cancer in humans, and thus one of skill in the art would not know how to use the protein produced by the claimed method.

In the first aspect, one of skill in the art cannot extrapolate the teaching of the specification to the enablement of the claims because the specification does not teach that the hWAPL polypeptideis expressed in any cancer cells. The prior art is replete with examples in which expression levels of mRNA are not correlated with expression levels of the encoded protein. For example, Fu et al (EMBO Journal, 1996, Vol. 15, pp. 4392-4401) teach that levels of p53 protein expression do not correlate with levels of p53 mRNA levels in blast cells taken from patients with acute myelogenous leukemia, said patients being without mutations in the p53 gene. Brennan et al (Journal of Autoimmunity, 1989, vol. 2 suppl., pp. 177-186) teaches that high levels of the mRNA for TNF-alpha were produced in synovial cells, but that levels of the TNF alpha protein were undetectable, and Zimmer (Cell Motility and the Cytoskeleton, 1991, vol. 20, pp. 325-337) teaches that there is no correlation between the mRNA level of calcium-modulated protein S100 alpha and levels of S100 alpha protein. Eriksson et al. (Diabetologia, 1992, vol. 35, pp. 143-147) teaches that no correlation is observed between levels of mRNA transcripts encoding the insulin-responsive glucose transporter and expression levels of the protein. Thus, observation of expression of mRNA does

not appear to be predictive of concomitant expression of protein. Thus, given the state of the art as reviewed above, data on the expression of mRNA encoding the hWAPL polypeptide in cancer cells does not allow one of skill in the art to predict that the hWAPL polypeptide is expressed in tumor cells or is involved in oncogenesis in vivo.

In the second aspect, one of skill in the art cannot extrapolate the teaching of the specification to enable the claim because the teaching in the specification that expression of the hWAPL protein in a cell line results in oncogenesis is not sufficient to establish that the hWAPL protein is associated with oncogenesis in vivo. In particular, Freshney (Culture of Animal Cells, A Manual of Basic Technique, Alan R. Liss, Inc., 1983, New York, p4) teaches that it is recognized in the art that there are many differences between cultured cells and their counterparts *in vivo*. These differences stem from the dissociation of cells from a three-dimensional geometry and their propagation on a two-dimensional substrate. Specific cell interactions characteristic of histology of the tissue are lost. The culture environment lacks the input of the nervous and endocrine systems involved in homeostatic regulation in vivo. Without this control, cellular metabolism may be more constant *in vitro* but may not be truly representative of the tissue from which the cells were derived. This has often led to tissue culture being regarded in a rather skeptical light (p. 4, see Major Differences *In Vitro*). Further, Dermer (Bio/Technology, 1994, 12:320) teaches that, a petri dish cancer is a poor representation of malignancy, with characteristics profoundly different from the human disease. Further, Dermer teaches that when a normal or malignant body cell adapts to immortal life in culture, it takes an evolutionary -type step that enables the new line to thrive in its artificial environment. This step transforms a cell from one that is stable and differentiated to one that is not, yet normal or malignant cells *in vivo* are not like that. The reference states that evidence of the contradictions between life on the bottom of a lab dish and in the body has been in the scientific literature for more than 30 years. Clearly it is well known in the art that cells in culture exhibit characteristics different from those *in vivo* and cannot duplicate the complex conditions of the *in vivo* environment involved in host-tumor and cell-cell interactions. Thus, given the state of the art as

reviewed above, data on the oncogenesis inducing potential of the expression of an hWAPL polypeptide in a cell line does not allow one of skill in the art to predict that the hWAPL polypeptide is expressed in tumor cells or is involved in oncogenesis.

It is clear that based on the state of the art, in the absence of experimental evidence, one skilled in the art would accept the assertion that the hWAPL protein is expressed in cancer cells or is involved in oncogenesis in vivo. The specification provides insufficient guidance with regard to this issue and provides no working examples which would provide guidance to one skilled in the art and no evidence has been provided which would allow one of skill in the art to predict that the hWAPL protein is expressed in cancer cells or is involved in oncogenesis in vivo. Thus, one of skill in the art would not know how to use the invention and practice of the invention would require undue experimentation.

6. Claims 1, 5, and 7 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated polynucleotide comprising the nucleotide sequence of SEQ ID NO:2, does not reasonably provide enablement for an isolated polynucleotide comprising a nucleotide sequence encoding the polypeptide of SEQ ID NO:1.

The claims are drawn to the following:

an isolated polynucleotide comprising a nucleotide sequence encoding the polypeptide represented by SEQ ID NO:1 (claim 1);

a recombinant vector comprising a polynucleotide of claim 1 or claim 2 (claim 5);

a transformed host cell produced by transforming a host cell with a recombinant vector comprising a polynucleotide of claim 1 or claim 2 (claim 7);

The specification teaches as set forth above.

The teaching of the specification cannot be extrapolated to enable the scope of the claims because one of skill in the art would not know how to use a polynucleotide that encodes a polypeptide of SEQ ID NO:1 because there is no showing a that polynucleotide other than SEQ ID NO:2 is overexpressed. Further, for the reasons set forth in Paragraph 6 above, one of skill in the art would not know how to use the encoded polypeptide if the polypeptide were not overexpressed in primary cancers because no function for SEQ ID NO:1 is taught in the specification. Thus, one of skill in the art would not know how to use a polynucleotide that encodes the polypeptide of SEQ ID NO:1, other than the polynucleotide of SEQ ID NO:2.

7. Claim 10 is rejected under 35 USC 112, first paragraph, as lacking an adequate written description in the specification.

The claims are drawn to a process for producing a recombinant oncogenic protein comprising an amino acid sequence of SEQ ID NO:1 comprising the steps of (i) transforming a host cell with a recombinant vector comprising a polynucleotide encoding an oncogenic protein with the amino acid sequence of SEQ ID NO:1, thereby creating a transformed cell, (ii) culturing the transformed cell whereby the transformed cell produces said recombinant oncogenic protein, and (iii) collecting said recombinant polypeptide from the culture.

Although drawn to the DNA arts, the finding in University of California v. Eli Lilly and Co., 119 F.3d 1559, 43 USPQ2d 1398 (Fed. Cir. 1997) and Enzo Biochem, Inc. V. Gen-Probe Inc. are relevant to the instant claims. The Federal Circuit addressed the application of the written description requirement to DNA-related inventions in University of California v. Eli Lilly and Co., 119 F.3d 1559, 43 USPQ2d 1398 (Fed. Cir. 1997). The court stated that "[a] written description of an invention involving a chemical genus, like a description of a chemical species, 'requires a precise definition, such as by structure, formula, [or] chemical name,' of the claimed subject matter sufficient to distinguish it from other materials." Id. At 1567, 43 USPQ2d at 1405. The court also stated that

> a generic statement such as "vertebrate insulin cDNA" or "mammalian insulin cDNA" without more, is not an adequate written description of the genus because it does not distinguish the genus from others, except by function. It does not specifically define any of the genes that fall within its definition. It does not define any structural features commonly possessed by members of the genus that distinguish them from others. One skilled in the art therefore cannot, as one can do with a fully described genus, visualize or recognize the identity of the members of the genus. A definition by function, as we have previously indicated, does not suffice to define the genus because it is only an indication of what the gene does, rather than what it is.

Id. At 1568, 43 USPQ2d at 1406. The court concluded that "naming a type of material generally known to exist, in the absence of knowledge as to what that material consists of, is not a description of that material." Id.

Finally, the court addressed the manner by which a genus of cDNAs might be described. "A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to the members of the genus, which features constitute a substantial portion of the genus." Id.

The Federal Circuit has recently clarified that a DNA molecule can be adequately described without disclosing its complete structure. See Enzo Biochem, Inc. V. Gen-Probe Inc., 296 F.3d 1316, 63 USPQ2d 1609 (Fed. Cir. 2002). The Enzo court adopted the standard that "the written description requirement can be met by 'show[ing] that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristics ....i.e., complete or partial structure, other physical and/or chemical properties, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics." Id. at 1324, 63 USPQ2d at 1613 (emphasis omitted, bracketed material in original).

The inventions at issue in Lilly and Enzo were DNA constructs per se, and the holdings of those cases are also applicable to claims such as those at issue here. A

disclosure that does not adequately describe a product itself logically cannot adequately describe a method of making that product.

Thus, the instant specification may provide an adequate written description of "an amino acid sequence of SEQ ID NO:1" per Lilly by structurally describing a representative number of species of "an amino acid sequence of SEQ ID NO:1" or by describing "structural features common to the members of the genus, which features constitute a substantial portion of the genus." Alternatively, per Enzo, the specification can show that the claimed invention is complete "by disclosure of sufficiently detailed, relevant identifying characteristics, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics."

In this case, the specification does not describe of "an amino acid sequence of SEQ ID NO:1", in the method of claim 10, in a manner that satisfies either the Lilly or Enzo standards. The specification does not provide the complete structure of any "an amino acid sequence of SEQ ID NO:1", nor does the specification provide any partial structure of such of "an amino acid sequence of SEQ ID NO:1", nor any physical or chemical characteristics of the of "an amino acid sequence of SEQ ID NO:1", nor any functional characteristics coupled with a known or disclosed correlation between structure and function, other than SEQ ID NO:1. Although the specification discloses a single polypeptide in SEQ ID NO:1, this does not provide a description of "an amino acid sequence of SEQ ID NO:1" of the claimed methods that would satisfy the standard set out in Enzo.

The specification also fails to describe the claimed of "an amino acid sequence of SEQ ID NO:1" by the test set out in Lilly. The specification describes only a single polypeptide, the polypeptide of SEQ ID NO:1. Therefore, it necessarily fails to describe a "representative number" of such species. In addition, the specification also does not describe "structural features common to the members of the genus, which features constitute a substantial portion of the genus."

Thus, the specification does not provide an adequate written description of "an amino acid sequence of SEQ ID NO:1". Since the specification fails to adequately describe the claimed product to be produced, it also fails to adequately describe the method of making that product.

Claim Rejections - 35 USC § 102

8. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

9. Claim 1, 2, 5, 7, and 15-17 are rejected under 35 U.S.C. 102(b) as being anticipated by Nagase et al. (1996, DNA Research 3:321-329), as evidenced by Genbank Accession No. D87450 .

The claims are drawn to the following:

an isolated polynucleotide comprising a nucleotide sequence encoding the polypeptide represented by SEQ ID NO:1 (claim 1);

an isolated polynucleotide comprising a nucleotide sequence encoding the polypeptide represented by SEQ ID NO:1 (claim 2), comprising the nucleotide sequence set forth in SEQ ID NO:2;

a recombinant vector comprising a polynucleotide of claim 1 or claim 2 (claim 5);

a transformed host cell produced by transforming a host cell with a recombinant vector comprising a polynucleotide of claim 1 or claim 2 (claim 7);

a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence of SEQ ID NO:2, wherein said polynucleotide has at least a length of 15 to 300 bases (claim 15);

a hybridization kit comprising the polynucleotide of claim 15 (claim 16);

a kit for detecting expression of mRNA which is translated into an oncogenic protein comprising the amino acid sequence of SEQ ID NO:1, comprising the polynucleotide of claim 15 (claim 17);

Nagase et al. disclosed the isolation and sequencing of a cDNA clone (KIAA0261) from the human immature myeloid cell line (abstract, page 325). As evidenced by the Genbank Accession No. D87450, and as shown by the attached sequence comparison between the nucleotide sequence of D87450 and the polypeptide sequence of SEQ ID NO:1 (Appendix A) and the attached sequence comparison between the nucleotide sequence of D87450 and the nucleotide sequence of SEQ ID NO:2, the isolated cDNA clone KIAA0261 comprises a sequence that is 100% identical to SEQ ID NO:2 and encodes a polypeptide having a sequence that is 100% identical to SEQ ID NO:1. It is noted that a cDNA clone comprising the sequence detailed in Genbank Accession No. D87450 would necessarily comprise "a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence of SEQ ID NO:2, wherein said polynucleotide has at least a length of 15 to 300 bases", as specified in claims 15-17. Thus, all of the claim limitations of claims 1, 2, 5, 7, and 15-17 are met.

Claim Rejections - 35 USC § 103

10. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) a patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious

at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

The factual inquiries set forth in *Graham* **v.** *John Deere Co.*, 383 U.S. 1, 148 USPQ 459 (1966), that are applied for establishing a background for determining obviousness under 35 U.S.C. 103(a) are summarized as follows:

1. Determining the scope and contents of the prior art.
2. Ascertaining the differences between the prior art and the claims at issue.
3. Resolving the level of ordinary skill in the pertinent art.
4. Considering objective evidence present in the application indicating obviousness or nonobviousness.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

11. Claims 16 and 17 are rejected under 35 U.S.C. 103(a) as being unpatentable over Nagase et al. (1996, DNA Research 3:321-329), as evidenced by Genbank Accession No. D87450.

The claims are drawn to the following:

a hybridization kit comprising a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence of SEQ ID NO:2, wherein said polynucleotide has at least a length of 15 to 300 bases the polynucleotide of claim 15 (claim 16);

a kit for detecting expression of mRNA which is translated into an oncogenic protein comprising the amino acid sequence of SEQ ID NO:1, comprising a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence of SEQ ID NO:2, wherein said polynucleotide has at least a length of 15 to 300 bases (claim 17).

Nagase et al. teaches as set forth above but does not specifically teach a kit comprising a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence of SEQ ID NO:2, wherein said polynucleotide has at least a length of 15 to 300 bases.

It would have been prima facie obvious to one of ordinary skill in the art at the time the invention was made to make a kit useful for the detection of KIAA0261 expression because Nagase teaches that the KIAA0261 was an expressed human RNA that encodes a protein. Official notice is taken that hybridization probes typically comprise at least 15 bases and that one of skill in the art would have had a reasonable expectation of success in making the kit because hybridization probes were well known in the art to be used successfully.

12. Claims 9 and 10 are rejected under 35 U.S.C. 103(a) as being unpatentable over Nagase et al. (1996, DNA Research 3:321-329), as evidenced by Genbank Accession No. D87450, in view of (Savvas, 1999, Protein Expression and Purification 17:183-202).

The claims are the following:

a process for producing a recombinant polypeptide or its salts comprising the amino acid sequence of SEQ ID NO:1 comprising the steps of:

transforming a host cell with a recombinant vector comprising a polynucleotide encoding the polypeptide represented by SEQ ID NO:1, thereby creating a transformed cell;

culturing the transformed cell whereby the transformed cell produces said polypeptide; and

collecting said recombinant polypeptide from the culture (claim 9);

and

a process for producing a recombinant oncogenic protein comprising an amino acid sequence of SEQ ID NO:1 comprising the steps of:

transforming a host cell with a recombinant vector comprising a polynucleotide encoding an oncogenic protein with the amino acid sequence of SEQ ID NO:1, thereby creating a transformed cell;

culturing the transformed cell whereby the transformed cell produces said recombinant oncogenic protein; and

collecting said recombinant polypeptide from the culture (claim 10);

Nagase teaches as set forth above, but does not specifically teach a process for producing protein comprising culturing transformed cells.

Savvas teaches that vectors for gene expression can be used to produce proteins from cultured mammalian cells (page 183) and that fusion proteins may be employed to facilitate the secretion of the protein and the isolation of the protein.

It would have been *prima facie* obvious to one of ordinary skill in the art at the time the invention was made to produce the protein encoded by the KIAA0261 using the methods described by Savvas. One of skill in the art would have been motivated to produce the protein to make antibodies to study the expression of the protein because Nagase teaches that the KIAA0261 protein was expressed in a variety of human tissues. One of skill in the art would have had a reasonable expectation of success in producing the protein because of the success taught by Savvas in producing protein from cloned genes.

13. Claim 18 is allowed. The closest prior art is Genbank Accession No. D87450 which discloses the sequence of SEQ ID NO:2. However, the reference does not disclose the specific primer set of the polynucleotides having the sequences of SEQ ID NO:8 and SEQ ID NO:9.

Conclusion

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Catherine M. Joyce whose telephone number is 571-272-3321. The examiner can normally be reached on Monday thru Friday, 10:15 - 6:45.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Jeffrey Siew can be reached on 571-272-0787. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

JEFFREY SIEW
SUPERVISORY PATENT EXAMINER

Catherine Joyce
Examiner
Art Unit 1642

Appendix A, PS. 2

```
RESULT 2
D87450
LOCUS       D87450                  6155 bp    mRNA    linear   PRI 06-OCT-2001
DEFINITION  Human mRNA for KIAA0261 gene, partial cds.
ACCESSION   D87450
VERSION     D87450.1  GI:1665788
KEYWORDS    KIAA0261.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayasi,Y.,
            Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N.
  TITLE     Prediction of the coding sequences of unidentified human genes. VI.
            The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
            analysis of cDNA clones from cell line KG-1 and brain
  JOURNAL   DNA Res. 3 (5), 321-329 (1996)
   PUBMED   9039502
REFERENCE   2  (bases 1 to 6155)
  AUTHORS   Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute;
            1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
FEATURES             Location/Qualifiers
     source          1. .6155
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HA7054"
                     /sex="male"
                     /cell_line="KG-1"
                     /cell_type="myeloblast"
                     /tissue_type="bone marrow"
                     /clone_lib="pBluescript II SK"
     gene            1. .6155
                     /gene="KIAA0261"
     CDS             <1. .3866
                     /gene="KIAA0261"
                     /note="Similar to D.melanogaster parallel sister
                     chromatids protein"
                     /codon_start=3
                     /protein_id="BAA13391.1"
                     /db_xref="GI:1665789"
                     /translation="KEVGAGSANGVEMVQGPVQTPALTIHRRKRRRSCPPNRASYLPK
                     AESLASLGSHLPALLSRARVPRPPAGRRERERRRRPVAKAPARLRGEYETGVKMTSRF
                     GKTYSRKGGNGSSKFDEVFSNKRTTLSTKWGETTFMAKLGQKRPNFKPDIQEIPKKPK
                     VEEESTGDPFGFDSDDESLPVSSKNLAQVKCSSYSESSEAAQLEEVTSVLEANSKISH
                     VVVEDTVVSDKCFPLEDTLLGKEKSTNRIVEDDASISSCNKLITSDKVENFHEEHEKN
                     SHHIHKNADDSTKKPNAETTVASEIKETNDTWNSQFGKRPESPSEISPIKGSVRTGLF
                     EWDNDFEDIRSEDCILSLDSDPLLEMKDDDFKNRLENLNEAIEEDIVQSVLRPTNCRT
                     YCRANKTKSSQGASNFDKLMDGTSQALAKANSESSKDGLNQAKKGGVSCGTSFRGTVG
                     RTRDYTVLHPSCLSVCNVTIQDTMERSMDEFTASTPADLGEAGRLRKKADIATSKTTT
                     RFRPSNTKSKKDVKLEFFGFEDHETGGDEGGSGSSNYKIKYFGFDDLSESEDDEDDDC
                     QVERKTSKKRTKTAPSPSLQPPPESNDNSQDSQSGTNNAENLDFTEDLPGVPESVKKP
                     INKQGDKSKENTRKIFSGPKRSPTKAVYNARHWNHPDSEELPGPPVVKPQSVTVRLSS
                     KEPNQKDDGVFKAPAPPSKVIKTVTIPTQPYQDIVTALKCRREDKELYTVVQHVKHFN
                     DVVEFGENQEFTDDIEYLLSGLKSTQPLNTRCLSVISLATKCAMPSFRMHLRAHGMVA
                     MVFKTLDDSQHHQNLSLCTAALMYILSRDRLNMDLDRASLDLMIRLLELEQDASSAKL
```

Appendix A, pg.2

LNEKDMNKIKEKIRRLCETVHNKHLDLENITTGHLAMETLLSLTSKRAGDWFKEELRL
LGGLDHIVDKVKECVDHLSRDEDEEKLVASLWGAERCLRVLESVTVHNPENQSYLIAY
KDSQLIVSSAKALQHCEELIQQYNRAEDSICLADSKPLPHQNVTNHVGKAVEDCMRAI
IGVLLNLTNDNEWGSTKTGEQDGLIGTALNCVLQVPKYLPQEQRFDIRVLGLGLLINL
VEYSARNRHCLVNMETSCSFDSSICSGEGDDSLRIGGQVHAVQALVQLFLERERAAQL
AESKTDELIKDAPTTQHDKSGEWQETSGEIQWVSTEKTDGTEEKHKKEEEDEELDLNK
ALQHAGKHMEDCIVASYTALLLGCLCQESPINVTTVREYLPEGDFSIMTEMLKKFLSF
MNLTCAVGTTGQKSISRVIEYLEHC"

ORIGIN

Alignment Scores:

Pred. No.:	0	Length:	6155
Score:	6195.00	Matches:	1190
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-758-562-1 (1-1190) x D87450 (1-6155)

```
Qy          1 MetThrSerArgPheGlyLysThrTyrSerArgLysGlyGlyAsnGlySerSerLysPhe 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 ATGACATCCAGATTTGGGAAAACATACAGTAGGAAAGGTGGAAATGGCAGTTCAAAATTC 353

Qy         21 AspGluValPheSerAsnLysArgThrThrLeuSerThrLysTrpGlyGluThrThrPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 GATGAAGTCTTTTCCAACAAACGGACTACCCTTAGCACAAAATGGGGAGAGACCACATTT 413

Qy         41 MetAlaLysLeuGlyGlnLysArgProAsnPheLysProAspIleGlnGluIleProLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 ATGGCTAAATTAGGGCAGAAGAGGCCCAATTTCAAACCAGATATCCAAGAAATTCCGAAG 473

Qy         61 LysProLysValGluGluGluSerThrGlyAspProPheGlyPheAspSerAspAspGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 AAACCTAAAGTGGAAGAAGAAAGTACTGGAGATCCTTTTGGATTTGATAGTGATGATGAG 533

Qy         81 SerLeuProValSerSerLysAsnLeuAlaGlnValLysCysSerSerTyrSerGluSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 TCTCTACCAGTTTCTTCAAAGAATTTAGCCCAGGTTAAGTGTTCCTCTTATTCAGAATCT 593

Qy        101 SerGluAlaAlaGlnLeuGluGluValThrSerValLeuGluAlaAsnSerLysIleSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 AGTGAAGCTGCTCAGTTGGAAGAGGTCACTTCAGTACTTGAAGCTAATAGCAAAATTAGT 653

Qy        121 HisValValValGluAspThrValValSerAspLysCysPheProLeuGluAspThrLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 CATGTGGTCGTTGAAGACACTGTCGTTTCTGATAAATGCTTCCCTTTGGAGGACACTTTA 713

Qy        141 LeuGlyLysGluLysSerThrAsnArgIleValGluAspAspAlaSerIleSerSerCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 CTTGGGAAAGAAAAGAGCACAAACCGAATTGTAGAAGATGATGCAAGCATAAGTAGCTGT 773

Qy        161 AsnLysLeuIleThrSerAspLysValGluAsnPheHisGluGluHisGluLysAsnSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 AATAAATTAATAACTTCAGATAAAGTGGAGAATTTTCATGAAGAACATGAAAAGAATAGT 833

Qy        181 HisHisIleHisLysAsnAlaAspAspSerThrLysLysProAsnAlaGluThrThrVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        834 CACCATATTCACAAAAATGCTGATGACAGTACTAAGAAACCCAATGCAGAAACTACAGTG 893

Qy        201 AlaSerGluIleLysGluThrAsnAspThrTrpAsnSerGlnPheGlyLysArgProGlu 220
```

Appendix A, pg. 3

```
Db        894 GCTTCTGAAATCAAGGAAACAAATGATACTTGGAACTCCCAGTTTGGGAAAAGGCCAGAA 953

Qy        221 SerProSerGluIleSerProIleLysGlySerValArgThrGlyLeuPheGluTrpAsp 240

Db        954 TCACCATCAGAAATATCTCCAATCAAGGGATCTGTTAGAACTGGTTTGTTTGAATGGGAT 1013

Qy        241 AsnAspPheGluAspIleArgSerGluAspCysIleLeuSerLeuAspSerAspProLeu 260

Db       1014 AATGATTTTGAAGATATCAGATCAGAAGACTGTATTTTAAGTTTGGATAGTGATCCCCTT 1073

Qy        261 LeuGluMetLysAspAspAspPheLysAsnArgLeuGluAsnLeuAsnGluAlaIleGlu 280

Db       1074 TTGGAGATGAAGGATGACGATTTTAAAAATCGATTGGAAAATCTGAATGAAGCCATTGAG 1133

Qy        281 GluAspIleValGlnSerValLeuArgProThrAsnCysArgThrTyrCysArgAlaAsn 300

Db       1134 GAAGATATTGTACAAAGTGTTCTTAGGCCAACCAACTGTAGGACGTACTGTAGGGCCAAT 1193

Qy        301 LysThrLysSerSerGlnGlyAlaSerAsnPheAspLysLeuMetAspGlyThrSerGln 320

Db       1194 AAAACGAAATCCTCCCAAGGAGCATCAAATTTTGATAAGCTGATGGACGGCACCAGTCAG 1253

Qy        321 AlaLeuAlaLysAlaAsnSerGluSerSerLysAspGlyLeuAsnGlnAlaLysLysGly 340

Db       1254 GCCTTAGCCAAAGCAAACAGTGAATCGAGTAAAGATGGCCTGAATCAGGCAAAGAAAGGG 1313

Qy        341 GlyValSerCysGlyThrSerPheArgGlyThrValGlyArgThrArgAspTyrThrVal 360

Db       1314 GGTGTAAGTTGTGGGACCAGTTTTAGAGGGACAGTTGGACGGACTAGAGATTACACTGTT 1373

Qy        361 LeuHisProSerCysLeuSerValCysAsnValThrIleGlnAspThrMetGluArgSer 380

Db       1374 TTACATCCATCTTGCTTGTCAGTTTGTAATGTTACCATACAGGATACTATGGAACGCAGC 1433

Qy        381 MetAspGluPheThrAlaSerThrProAlaAspLeuGlyGluAlaGlyArgLeuArgLys 400

Db       1434 ATGGATGAGTTCACTGCATCCACTCCTGCAGATTTGGGAGAAGCTGGTCGTCTCAGAAAA 1493

Qy        401 LysAlaAspIleAlaThrSerLysThrThrThrArgPheArgProSerAsnThrLysSer 420

Db       1494 AAGGCAGATATTGCAACTTCTAAGACTACTACTAGATTTCGACCTAGTAATACTAAATCC 1553

Qy        421 LysLysAspValLysLeuGluPhePheGlyPheGluAspHisGluThrGlyGlyAspGlu 440

Db       1554 AAAAAGGATGTTAAACTTGAATTTTTTGGTTTTGAAGATCATGAGACAGGAGGTGATGAA 1613

Qy        441 GlyGlySerGlySerSerAsnTyrLysIleLysTyrPheGlyPheAspAspLeuSerGlu 460

Db       1614 GGAGGTTCTGGAAGTTCTAATTACAAAATTAAGTATTTTGGCTTTGATGATCTCAGTGAA 1673

Qy        461 SerGluAspAspGluAspAspAspCysGlnValGluArgLysThrSerLysLysArgThr 480

Db       1674 AGCGAAGATGATGAAGATGATGACTGTCAAGTAGAAAGAAAGACAAGCAAAAAAAGAACT 1733

Qy        481 LysThrAlaProSerProSerLeuGlnProProProGluSerAsnAspAsnSerGlnAsp 500

Db       1734 AAAACAGCTCCATCACCCTCCTTGCAGCCTCCCCCAGAAAGCAATGATAATTCCCAGGAC 1793

Qy        501 SerGlnSerGlyThrAsnAsnAlaGluAsnLeuAspPheThrGluAspLeuProGlyVal 520
```

Appendix A, Pg. 4

```
Db       1794 AGTCAGTCTGGTACTAACAATGCAGAAAACTTGGATTTTACAGAGGACTTGCCTGGTGTG 1853

Qy        521 ProGluSerValLysLysProIleAsnLysGlnGlyAspLysSerLysGluAsnThrArg 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1854 CCTGAAAGTGTGAAGAAGCCCATAAATAAACAAGGAGATAAATCAAAGGAAAATACCAGA 1913

Qy        541 LysIlePheSerGlyProLysArgSerProThrLysAlaValTyrAsnAlaArgHisTrp 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1914 AAGATTTTTAGTGGCCCCAAACGGTCACCCACAAAAGCTGTATATAATGCCAGACATTGG 1973

Qy        561 AsnHisProAspSerGluGluLeuProGlyProProValValLysProGlnSerValThr 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1974 AATCATCCAGATTCAGAAGAACTGCCTGGGCCACCAGTAGTAAAACCTCAGAGTGTCACA 2033

Qy        581 ValArgLeuSerSerLysGluProAsnGlnLysAspAspGlyValPheLysAlaProAla 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2034 GTGAGGCTGTCTTCAAAGGAACCAAATCAAAAAGATGATGGAGTTTTTAAGGCTCCTGCA 2093

Qy        601 ProProSerLysValIleLysThrValThrIleProThrGlnProTyrGlnAspIleVal 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2094 CCACCATCCAAAGTGATAAAAACTGTGACAATACCTACTCAGCCCTACCAAGATATAGTT 2153

Qy        621 ThrAlaLeuLysCysArgArgGluAspLysGluLeuTyrThrValValGlnHisValLys 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2154 ACTGCACTGAAATGCAGACGAGAAGACAAAGAATTATATACTGTTGTTCAGCACGTGAAG 2213

Qy        641 HisPheAsnAspValValGluPheGlyGluAsnGlnGluPheThrAspAspIleGluTyr 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2214 CACTTCAACGATGTTGTAGAATTTGGTGAAAATCAAGAGTTCACTGATGACATTGAGTAC 2273

Qy        661 LeuLeuSerGlyLeuLysSerThrGlnProLeuAsnThrArgCysLeuSerValIleSer 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2274 TTGTTAAGTGGCTTAAAGAGCACTCAGCCTCTAAACACACGTTGCCTTAGTGTTATTAGC 2333

Qy        681 LeuAlaThrLysCysAlaMetProSerPheArgMetHisLeuArgAlaHisGlyMetVal 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2334 TTGGCTACTAAATGTGCCATGCCCAGTTTTCGAATGCACCTGAGAGCACATGGGATGGTA 2393

Qy        701 AlaMetValPheLysThrLeuAspAspSerGlnHisHisGlnAsnLeuSerLeuCysThr 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2394 GCAATGGTCTTTAAAACCTTGGATGATTCCCAGCACCATCAGAATCTGTCCCTCTGTACA 2453

Qy        721 AlaAlaLeuMetTyrIleLeuSerArgAspArgLeuAsnMetAspLeuAspArgAlaSer 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2454 GCTGCCCTCATGTATATACTGAGTAGAGATCGTTTGAACATGGATCTTGATAGAGCTAGC 2513

Qy        741 LeuAspLeuMetIleArgLeuLeuGluLeuGluGlnAspAlaSerSerAlaLysLeuLeu 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2514 TTAGATCTAATGATTCGACTTTTGGAACTGGAACAAGATGCTTCATCAGCCAAGCTACTG 2573

Qy        761 AsnGluLysAspMetAsnLysIleLysGluLysIleArgArgLeuCysGluThrValHis 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2574 AATGAAAAAGACATGAACAAAATTAAAGAAAAAATCCGAAGGCTCTGTGAAACTGTACAC 2633

Qy        781 AsnLysHisLeuAspLeuGluAsnIleThrThrGlyHisLeuAlaMetGluThrLeuLeu 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2634 AACAAGCATCTTGATCTAGAAAATATAACGACTGGGCATTTAGCTATGGAGACATTATTA 2693

Qy        801 SerLeuThrSerLysArgAlaGlyAspTrpPheLysGluGluLeuArgLeuLeuGlyGly 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2694 TCCCTTACTTCTAAACGAGCAGGAGACTGGTTTAAAGAAGAACTCCGGCTTTTGGGTGGT 2753
```

Appendix A, pg. 5

```
Qy       821 LeuAspHisIleValAspLysValLysGluCysValAspHisLeuSerArgAspGluAsp 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2754 CTGGATCATATTGTAGATAAAGTAAAAGAATGTGTGGATCATTTAAGTAGAGATGAGGAT 2813

Qy       841 GluGluLysLeuValAlaSerLeuTrpGlyAlaGluArgCysLeuArgValLeuGluSer 860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2814 GAAGAGAAACTGGTAGCCTCACTATGGGGAGCAGAGAGATGTTTACGAGTTTTAGAAAGT 2873

Qy       861 ValThrValHisAsnProGluAsnGlnSerTyrLeuIleAlaTyrLysAspSerGlnLeu 880
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2874 GTAACTGTGCATAATCCCGAAAATCAAAGCTACTTGATAGCATATAAAGATTCCCAACTT 2933

Qy       881 IleValSerSerAlaLysAlaLeuGlnHisCysGluGluLeuIleGlnGlnTyrAsnArg 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2934 ATTGTTTCATCAGCTAAAGCATTACAGCATTGTGAAGAACTGATTCAGCAGTACAACCGT 2993

Qy       901 AlaGluAspSerIleCysLeuAlaAspSerLysProLeuProHisGlnAsnValThrAsn 920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2994 GCTGAGGACAGCATATGCTTAGCTGACAGTAAGCCTCTGCCTCACCAGAATGTAACTAAC 3053

Qy       921 HisValGlyLysAlaValGluAspCysMetArgAlaIleIleGlyValLeuLeuAsnLeu 940
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3054 CATGTAGGCAAAGCAGTGGAGGACTGCATGAGGGCCATCATCGGGGTGTTGCTTAATTTA 3113

Qy       941 ThrAsnAspAsnGluTrpGlySerThrLysThrGlyGluGlnAspGlyLeuIleGlyThr 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3114 ACTAATGATAATGAGTGGGGCAGCACCAAAACAGGAGAGCAGGACGGTCTCATAGGCACA 3173

Qy       961 AlaLeuAsnCysValLeuGlnValProLysTyrLeuProGlnGluGlnArgPheAspIle 980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3174 GCGCTGAACTGTGTGCTTCAGGTTCCAAAGTACCTACCTCAGGAGCAGAGATTTGATATT 3233

Qy       981 ArgValLeuGlyLeuGlyLeuLeuIleAsnLeuValGluTyrSerAlaArgAsnArgHis 1000
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3234 CGAGTGCTGGGCTTAGGTCTGCTGATAAATCTAGTGGAGTATAGTGCTCGGAATCGGCAC 3293

Qy      1001 CysLeuValAsnMetGluThrSerCysSerPheAspSerSerIleCysSerGlyGluGly 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3294 TGTCTTGTCAACATGGAAACATCGTGCTCTTTTGATTCTTCCATCTGTAGTGGAGAAGGG 3353

Qy      1021 AspAspSerLeuArgIleGlyGlyGlnValHisAlaValGlnAlaLeuValGlnLeuPhe 1040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3354 GATGATAGTTTAAGGATAGGTGGACAAGTTCATGCTGTCCAGGCTTTAGTGCAGCTATTC 3413

Qy      1041 LeuGluArgGluArgAlaAlaGlnLeuAlaGluSerLysThrAspGluLeuIleLysAsp 1060
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3414 CTTGAGCGAGAGCGGGCAGCCCAGCTAGCAGAAAGTAAAACAGATGAGTTGATCAAAGAT 3473

Qy      1061 AlaProThrThrGlnHisAspLysSerGlyGluTrpGlnGluThrSerGlyGluIleGln 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3474 GCTCCCACCACTCAGCATGATAAGAGTGGAGAGTGGCAAGAAACAAGTGGAGAAATACAG 3533

Qy      1081 TrpValSerThrGluLysThrAspGlyThrGluGluLysHisLysLysGluGluGluAsp 1100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3534 TGGGTGTCAACTGAAAAGACTGATGGTACAGAAGAGAAACATAAGAAGGAGGAGGAGGAT 3593

Qy      1101 GluGluLeuAspLeuAsnLysAlaLeuGlnHisAlaGlyLysHisMetGluAspCysIle 1120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3594 GAAGAACTTGACCTCAATAAAGCCCTTCAGCATGCCGGCAAACACATGGAGGATTGCATT 3653
```

Appendix A, pg. 6

```
Qy       1121 ValAlaSerTyrThrAlaLeuLeuLeuGlyCysLeuCysGlnGluSerProIleAsnVal 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3654 GTGGCCTCCTACACGGCACTACTTCTTGGGTGTCTCTGCCAGGAAAGTCCAATCAATGTA 3713

Qy       1141 ThrThrValArgGluTyrLeuProGluGlyAspPheSerIleMetThrGluMetLeuLys 1160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3714 ACCACTGTGCGGGAATATCTGCCAGAAGGAGACTTTTCAATAATGACAGAGATGCTCAAA 3773

Qy       1161 LysPheLeuSerPheMetAsnLeuThrCysAlaValGlyThrThrGlyGlnLysSerIle 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3774 AAATTTTTGAGTTTTATGAATCTCACTTGTGCTGTTGGAACAACTGGCCAGAAATCTATC 3833

Qy       1181 SerArgValIleGluTyrLeuGluHisCys 1190
              ||||||||||||||||||||||||||||||
Db       3834 TCTAGAGTGATTGAATATTTGGAACATTGC 3863
```

Appendix B, PS-1

```
RESULT 2
D87450
LOCUS       D87450                  6155 bp    mRNA    linear   PRI 06-OCT-2001
DEFINITION  Human mRNA for KIAA0261 gene, partial cds.
ACCESSION   D87450
VERSION     D87450.1  GI:1665788
KEYWORDS    KIAA0261.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayasi,Y.,
            Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N.
  TITLE     Prediction of the coding sequences of unidentified human genes. VI.
            The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
            analysis of cDNA clones from cell line KG-1 and brain
  JOURNAL   DNA Res. 3 (5), 321-329 (1996)
   PUBMED   9039502
REFERENCE   2  (bases 1 to 6155)
  AUTHORS   Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute;
            1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
FEATURES             Location/Qualifiers
     source          1. .6155
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HA7054"
                     /sex="male"
                     /cell_line="KG-1"
                     /cell_type="myeloblast"
                     /tissue_type="bone marrow"
                     /clone_lib="pBluescript II SK"
     gene            1. .6155
                     /gene="KIAA0261"
     CDS             <1. .3866
                     /gene="KIAA0261"
                     /note="Similar to D.melanogaster parallel sister
                     chromatids protein"
                     /codon_start=3
                     /protein_id="BAA13391.1"
                     /db_xref="GI:1665789"
                     /translation="KEVGAGSANGVEMVQGPVQTPALTIHRRKRRRSCPPNRASYLPK
                     AESLASLGSHLPALLSRARVPRPPAGRRERERRRRPVAKAPARLRGEYETGVKMTSRF
                     GKTYSRKGGNGSSKFDEVFSNKRTTLSTKWGETTFMAKLGQKRPNFKPDIQEIPKKPK
                     VEEESTGDPFGFDSDDESLPVSSKNLAQVKCSSYSESSEAAQLEEVTSVLEANSKISH
                     VVVEDTVVSDKCFPLEDTLLGKEKSTNRIVEDDASISSCNKLITSDKVENFHEEHEKN
                     SHHIHKNADDSTKKPNAETTVASEIKETNDTWNSQFGKRPESPSEISPIKGSVRTGLF
                     EWDNDFEDIRSEDCILSLDSDPLLEMKDDDFKNRLENLNEAIEEDIVQSVLRPTNCRT
                     YCRANKTKSSQGASNFDKLMDGTSQALAKANSESSKDGLNQAKKGGVSCGTSFRGTVG
                     RTRDYTVLHPSCLSVCNVTIQDTMERSMDEFTASTPADLGEAGRLRKKADIATSKTTT
                     RFRPSNTKSKKDVKLEFFGFEDHETGGDEGGSGSSNYKIKYFGFDDLSESEDDEDDDC
                     QVERKTSKKRTKTAPSPSLQPPPESNDNSQDSQSGTNNAENLDFTEDLPGVPESVKKP
                     INKQGDKSKENTRKIFSGPKRSPTKAVYNARHWNHPDSEELPGPPVVKPQSVTVRLSS
                     KEPNQKDDGVFKAPAPPSKVIKTVTIPTQPYQDIVTALKCRREDKELYTVVQHVKHFN
                     DVVEFGENQEFTDDIEYLLSGLKSTQPLNTRCLSVISLATKCAMPSFRMHLRAHGMVA
                     MVFKTLDDSQHHQNLSLCTAALMYILSRDRLNMDLDRASLDLMIRLLELEQDASSAKL
```

Appendix B, pg. 2

LNEKDMNKIKEKIRRLCETVHNKHLDLENITTGHLAMETLLSLTSKRAGDWFKEELRL
LGGLDHIVDKVKECVDHLSRDEDEEKLVASLWGAERCLRVLESVTVHNPENQSYLIAY
KDSQLIVSSAKALQHCEELIQQYNRAEDSICLADSKPLPHQNVTNHVGKAVEDCMRAI
IGVLLNLTNDNEWGSTKTGEQDGLIGTALNCVLQVPKYLPQEQRFDIRVLGLGLLINL
VEYSARNRHCLVNMETSCSFDSSICSGEGDDSLRIGGQVHAVQALVQLFLERERAAQL
AESKTDELIKDAPTTQHDKSGEWQETSGEIQWVSTEKTDGTEEKHKKEEEDEELDLNK
ALQHAGKHMEDCIVASYTALLLGCLCQESPINVTTVREYLPEGDFSIMTEMLKKFLSF
MNLTCAVGTTGQKSISRVIEYLEHC"

ORIGIN

Query Match 100.0%; Score 3570; DB 5; Length 6155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGACATCCAGATTTGGGAAAACATACAGTAGGAAAGGTGGAAATGGCAGTTCAAAATTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 ATGACATCCAGATTTGGGAAAACATACAGTAGGAAAGGTGGAAATGGCAGTTCAAAATTC 353

Qy         61 GATGAAGTCTTTTTCCAACAAACGGACTACCCTTAGCACAAAATGGGGAGAGACCACATTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 GATGAAGTCTTTTTCCAACAAACGGACTACCCTTAGCACAAAATGGGGAGAGACCACATTT 413

Qy        121 ATGGCTAAATTAGGGCAGAAGAGGCCCAATTTCAAACCAGATATCCAAGAAATTCCGAAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 ATGGCTAAATTAGGGCAGAAGAGGCCCAATTTCAAACCAGATATCCAAGAAATTCCGAAG 473

Qy        181 AAACCTAAAGTGGAAGAAGAAAGTACTGGAGATCCTTTTGGATTTGATAGTGATGATGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 AAACCTAAAGTGGAAGAAGAAAGTACTGGAGATCCTTTTGGATTTGATAGTGATGATGAG 533

Qy        241 TCTCTACCAGTTTCTTCAAAGAATTTAGCCCAGGTTAAGTGTTCCTCTTATTCAGAATCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 TCTCTACCAGTTTCTTCAAAGAATTTAGCCCAGGTTAAGTGTTCCTCTTATTCAGAATCT 593

Qy        301 AGTGAAGCTGCTCAGTTGGAAGAGGTCACTTCAGTACTTGAAGCTAATAGCAAAATTAGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 AGTGAAGCTGCTCAGTTGGAAGAGGTCACTTCAGTACTTGAAGCTAATAGCAAAATTAGT 653

Qy        361 CATGTGGTCGTTGAAGACACTGTCGTTTCTGATAAATGCTTCCCTTTGGAGGACACTTTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 CATGTGGTCGTTGAAGACACTGTCGTTTCTGATAAATGCTTCCCTTTGGAGGACACTTTA 713

Qy        421 CTTGGGAAAGAAAAGAGCACAAACCGAATTGTAGAAGATGATGCAAGCATAAGTAGCTGT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 CTTGGGAAAGAAAAGAGCACAAACCGAATTGTAGAAGATGATGCAAGCATAAGTAGCTGT 773

Qy        481 AATAAATTAATAACTTCAGATAAAGTGGAGAATTTTCATGAAGAACATGAAAAGAATAGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 AATAAATTAATAACTTCAGATAAAGTGGAGAATTTTCATGAAGAACATGAAAAGAATAGT 833

Qy        541 CACCATATTCACAAAAATGCTGATGACAGTACTAAGAAACCCAATGCAGAAACTACAGTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        834 CACCATATTCACAAAAATGCTGATGACAGTACTAAGAAACCCAATGCAGAAACTACAGTG 893

Qy        601 GCTTCTGAAATCAAGGAAACAAATGATACTTGGAACTCCCAGTTTGGGAAAAGGCCAGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        894 GCTTCTGAAATCAAGGAAACAAATGATACTTGGAACTCCCAGTTTGGGAAAAGGCCAGAA 953

Qy        661 TCACCATCAGAAATATCTCCAATCAAGGGATCTGTTAGAACTGGTTTGTTTGAATGGGAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        954 TCACCATCAGAAATATCTCCAATCAAGGGATCTGTTAGAACTGGTTTGTTTGAATGGGAT 1013
```

Appendix B, PS.2

```
Qy       721 AATGATTTTGAAGATATCAGATCAGAAGACTGTATTTTAAGTTTGGATAGTGATCCCCTT 780
Db      1014 AATGATTTTGAAGATATCAGATCAGAAGACTGTATTTTAAGTTTGGATAGTGATCCCCTT 1073

Qy       781 TTGGAGATGAAGGATGACGATTTTAAAAATCGATTGGAAAATCTGAATGAAGCCATTGAG 840
Db      1074 TTGGAGATGAAGGATGACGATTTTAAAAATCGATTGGAAAATCTGAATGAAGCCATTGAG 1133

Qy       841 GAAGATATTGTACAAAGTGTTCTTAGGCCAACCAACTGTAGGACGTACTGTAGGGCCAAT 900
Db      1134 GAAGATATTGTACAAAGTGTTCTTAGGCCAACCAACTGTAGGACGTACTGTAGGGCCAAT 1193

Qy       901 AAAACGAAATCCTCCCAAGGAGCATCAAATTTTGATAAGCTGATGGACGGCACCAGTCAG 960
Db      1194 AAAACGAAATCCTCCCAAGGAGCATCAAATTTTGATAAGCTGATGGACGGCACCAGTCAG 1253

Qy       961 GCCTTAGCCAAAGCAAACAGTGAATCGAGTAAAGATGGCCTGAATCAGGCAAAGAAAGGG 1020
Db      1254 GCCTTAGCCAAAGCAAACAGTGAATCGAGTAAAGATGGCCTGAATCAGGCAAAGAAAGGG 1313

Qy      1021 GGTGTAAGTTGTGGGACCAGTTTTAGAGGGACAGTTGGACGGACTAGAGATTACACTGTT 1080
Db      1314 GGTGTAAGTTGTGGGACCAGTTTTAGAGGGACAGTTGGACGGACTAGAGATTACACTGTT 1373

Qy      1081 TTACATCCATCTTGCTTGTCAGTTTGTAATGTTACCATACAGGATACTATGGAACGCAGC 1140
Db      1374 TTACATCCATCTTGCTTGTCAGTTTGTAATGTTACCATACAGGATACTATGGAACGCAGC 1433

Qy      1141 ATGGATGAGTTCACTGCATCCACTCCTGCAGATTTGGGAGAAGCTGGTCGTCTCAGAAAA 1200
Db      1434 ATGGATGAGTTCACTGCATCCACTCCTGCAGATTTGGGAGAAGCTGGTCGTCTCAGAAAA 1493

Qy      1201 AAGGCAGATATTGCAACTTCTAAGACTACTACTAGATTTCGACCTAGTAATACTAAATCC 1260
Db      1494 AAGGCAGATATTGCAACTTCTAAGACTACTACTAGATTTCGACCTAGTAATACTAAATCC 1553

Qy      1261 AAAAAGGATGTTAAACTTGAATTTTTTGGTTTTGAAGATCATGAGACAGGAGGTGATGAA 1320
Db      1554 AAAAAGGATGTTAAACTTGAATTTTTTGGTTTTGAAGATCATGAGACAGGAGGTGATGAA 1613

Qy      1321 GGAGGTTCTGGAAGTTCTAATTACAAAATTAAGTATTTTGGCTTTGATGATCTCAGTGAA 1380
Db      1614 GGAGGTTCTGGAAGTTCTAATTACAAAATTAAGTATTTTGGCTTTGATGATCTCAGTGAA 1673

Qy      1381 AGCGAAGATGATGAAGATGATGACTGTCAAGTAGAAAGAAAGACAAGCAAAAAAAGAACT 1440
Db      1674 AGCGAAGATGATGAAGATGATGACTGTCAAGTAGAAAGAAAGACAAGCAAAAAAAGAACT 1733

Qy      1441 AAAACAGCTCCATCACCCTCCTTGCAGCCTCCCCCAGAAAGCAATGATAATTCCCAGGAC 1500
Db      1734 AAAACAGCTCCATCACCCTCCTTGCAGCCTCCCCCAGAAAGCAATGATAATTCCCAGGAC 1793

Qy      1501 AGTCAGTCTGGTACTAACAATGCAGAAAACTTGGATTTTACAGAGGACTTGCCTGGTGTG 1560
Db      1794 AGTCAGTCTGGTACTAACAATGCAGAAAACTTGGATTTTACAGAGGACTTGCCTGGTGTG 1853

Qy      1561 CCTGAAAGTGTGAAGAAGCCCATAAATAAACAAGGAGATAAATCAAAGGAAAATACCAGA 1620
Db      1854 CCTGAAAGTGTGAAGAAGCCCATAAATAAACAAGGAGATAAATCAAAGGAAAATACCAGA 1913
```

Appendix B, p.4

```
Qy      1621 AAGATTTTTTAGTGGCCCCAAACGGTCACCCACAAAAGCTGTATATAATGCCAGACATTGG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1914 AAGATTTTTTAGTGGCCCCAAACGGTCACCCACAAAAGCTGTATATAATGCCAGACATTGG 1973

Qy      1681 AATCATCCAGATTCAGAAGAACTGCCTGGGCCACCAGTAGTAAAACCTCAGAGTGTCACA 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1974 AATCATCCAGATTCAGAAGAACTGCCTGGGCCACCAGTAGTAAAACCTCAGAGTGTCACA 2033

Qy      1741 GTGAGGCTGTCTTCAAAGGAACCAAATCAAAAAGATGATGGAGTTTTTAAGGCTCCTGCA 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2034 GTGAGGCTGTCTTCAAAGGAACCAAATCAAAAAGATGATGGAGTTTTTAAGGCTCCTGCA 2093

Qy      1801 CCACCATCCAAAGTGATAAAAACTGTGACAATACCTACTCAGCCCTACCAAGATATAGTT 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2094 CCACCATCCAAAGTGATAAAAACTGTGACAATACCTACTCAGCCCTACCAAGATATAGTT 2153

Qy      1861 ACTGCACTGAAATGCAGACGAGAAGACAAAGAATTATATACTGTTGTTCAGCACGTGAAG 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2154 ACTGCACTGAAATGCAGACGAGAAGACAAAGAATTATATACTGTTGTTCAGCACGTGAAG 2213

Qy      1921 CACTTCAACGATGTTGTAGAATTTGGTGAAAATCAAGAGTTCACTGATGACATTGAGTAC 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2214 CACTTCAACGATGTTGTAGAATTTGGTGAAAATCAAGAGTTCACTGATGACATTGAGTAC 2273

Qy      1981 TTGTTAAGTGGCTTAAAGAGCACTCAGCCTCTAAACACACGTTGCCTTAGTGTTATTAGC 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2274 TTGTTAAGTGGCTTAAAGAGCACTCAGCCTCTAAACACACGTTGCCTTAGTGTTATTAGC 2333

Qy      2041 TTGGCTACTAAATGTGCCATGCCCAGTTTTCGAATGCACCTGAGAGCACATGGGATGGTA 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2334 TTGGCTACTAAATGTGCCATGCCCAGTTTTCGAATGCACCTGAGAGCACATGGGATGGTA 2393

Qy      2101 GCAATGGTCTTTAAAACCTTGGATGATTCCCAGCACCATCAGAATCTGTCCCTCTGTACA 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2394 GCAATGGTCTTTAAAACCTTGGATGATTCCCAGCACCATCAGAATCTGTCCCTCTGTACA 2453

Qy      2161 GCTGCCCTCATGTATATACTGAGTAGAGATCGTTTGAACATGGATCTTGATAGAGCTAGC 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2454 GCTGCCCTCATGTATATACTGAGTAGAGATCGTTTGAACATGGATCTTGATAGAGCTAGC 2513

Qy      2221 TTAGATCTAATGATTCGACTTTTGGAACTGGAACAAGATGCTTCATCAGCCAAGCTACTG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2514 TTAGATCTAATGATTCGACTTTTGGAACTGGAACAAGATGCTTCATCAGCCAAGCTACTG 2573

Qy      2281 AATGAAAAAGACATGAACAAAATTAAAGAAAAAATCCGAAGGCTCTGTGAAACTGTACAC 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2574 AATGAAAAAGACATGAACAAAATTAAAGAAAAAATCCGAAGGCTCTGTGAAACTGTACAC 2633

Qy      2341 AACAAGCATCTTGATCTAGAAAATATAACGACTGGGCATTTAGCTATGGAGACATTATTA 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2634 AACAAGCATCTTGATCTAGAAAATATAACGACTGGGCATTTAGCTATGGAGACATTATTA 2693

Qy      2401 TCCCTTACTTCTAAACGAGCAGGAGACTGGTTTAAAGAAGAACTCCGGCTTTTGGGTGGT 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2694 TCCCTTACTTCTAAACGAGCAGGAGACTGGTTTAAAGAAGAACTCCGGCTTTTGGGTGGT 2753

Qy      2461 CTGGATCATATTGTAGATAAAGTAAAAGAATGTGTGGATCATTTAAGTAGAGATGAGGAT 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2754 CTGGATCATATTGTAGATAAAGTAAAAGAATGTGTGGATCATTTAAGTAGAGATGAGGAT 2813

Qy      2521 GAAGAGAAACTGGTAGCCTCACTATGGGGAGCAGAGAGATGTTTACGAGTTTTAGAAAGT 2580
```

Appendix B, pg. 5

```
Db      2814 GAAGAGAAACTGGTAGCCTCACTATGGGGAGCAGAGAGATGTTTACGAGTTTTAGAAAGT 2873

Qy      2581 GTAACTGTGCATAATCCCGAAAATCAAAGCTACTTGATAGCATATAAAGATTCCCAACTT 2640

Db      2874 GTAACTGTGCATAATCCCGAAAATCAAAGCTACTTGATAGCATATAAAGATTCCCAACTT 2933

Qy      2641 ATTGTTTCATCAGCTAAAGCATTACAGCATTGTGAAGAACTGATTCAGCAGTACAACCGT 2700

Db      2934 ATTGTTTCATCAGCTAAAGCATTACAGCATTGTGAAGAACTGATTCAGCAGTACAACCGT 2993

Qy      2701 GCTGAGGACAGCATATGCTTAGCTGACAGTAAGCCTCTGCCTCACCAGAATGTAACTAAC 2760

Db      2994 GCTGAGGACAGCATATGCTTAGCTGACAGTAAGCCTCTGCCTCACCAGAATGTAACTAAC 3053

Qy      2761 CATGTAGGCAAAGCAGTGGAGGACTGCATGAGGGCCATCATCGGGGTGTTGCTTAATTTA 2820

Db      3054 CATGTAGGCAAAGCAGTGGAGGACTGCATGAGGGCCATCATCGGGGTGTTGCTTAATTTA 3113

Qy      2821 ACTAATGATAATGAGTGGGGCAGCACCAAAACAGGAGAGCAGGACGGTCTCATAGGCACA 2880

Db      3114 ACTAATGATAATGAGTGGGGCAGCACCAAAACAGGAGAGCAGGACGGTCTCATAGGCACA 3173

Qy      2881 GCGCTGAACTGTGTGCTTCAGGTTCCAAAGTACCTACCTCAGGAGCAGAGATTTGATATT 2940

Db      3174 GCGCTGAACTGTGTGCTTCAGGTTCCAAAGTACCTACCTCAGGAGCAGAGATTTGATATT 3233

Qy      2941 CGAGTGCTGGGCTTAGGTCTGCTGATAAATCTAGTGGAGTATAGTGCTCGGAATCGGCAC 3000

Db      3234 CGAGTGCTGGGCTTAGGTCTGCTGATAAATCTAGTGGAGTATAGTGCTCGGAATCGGCAC 3293

Qy      3001 TGTCTTGTCAACATGGAAACATCGTGCTCTTTTGATTCTTCCATCTGTAGTGGAGAAGGG 3060

Db      3294 TGTCTTGTCAACATGGAAACATCGTGCTCTTTTGATTCTTCCATCTGTAGTGGAGAAGGG 3353

Qy      3061 GATGATAGTTTAAGGATAGGTGGACAAGTTCATGCTGTCCAGGCTTTAGTGCAGCTATTC 3120

Db      3354 GATGATAGTTTAAGGATAGGTGGACAAGTTCATGCTGTCCAGGCTTTAGTGCAGCTATTC 3413

Qy      3121 CTTGAGCGAGAGCGGGCAGCCCAGCTAGCAGAAAGTAAAACAGATGAGTTGATCAAAGAT 3180

Db      3414 CTTGAGCGAGAGCGGGCAGCCCAGCTAGCAGAAAGTAAAACAGATGAGTTGATCAAAGAT 3473

Qy      3181 GCTCCCACCACTCAGCATGATAAGAGTGGAGAGTGGCAAGAAACAAGTGGAGAAATACAG 3240

Db      3474 GCTCCCACCACTCAGCATGATAAGAGTGGAGAGTGGCAAGAAACAAGTGGAGAAATACAG 3533

Qy      3241 TGGGTGTCAACTGAAAAGACTGATGGTACAGAAGAGAAACATAAGAAGGAGGAGGAGGAT 3300

Db      3534 TGGGTGTCAACTGAAAAGACTGATGGTACAGAAGAGAAACATAAGAAGGAGGAGGAGGAT 3593

Qy      3301 GAAGAACTTGACCTCAATAAAGCCCTTCAGCATGCCGGCAAACACATGGAGGATTGCATT 3360

Db      3594 GAAGAACTTGACCTCAATAAAGCCCTTCAGCATGCCGGCAAACACATGGAGGATTGCATT 3653

Qy      3361 GTGGCCTCCTACACGGCACTACTTCTTGGGTGTCTCTGCCAGGAAAGTCCAATCAATGTA 3420

Db      3654 GTGGCCTCCTACACGGCACTACTTCTTGGGTGTCTCTGCCAGGAAAGTCCAATCAATGTA 3713

Qy      3421 ACCACTGTGCGGGAATATCTGCCAGAAGGAGACTTTTCAATAATGACAGAGATGCTCAAA 3480
```

Appendix B, pg. 6

```
Db       3714 ACCACTGTGCGGGAATATCTGCCAGAAGGAGACTTTTCAATAATGACAGAGATGCTCAAA 3773

Qy       3481 AAATTTTTGAGTTTTATGAATCTCACTTGTGCTGTTGGAACAACTGGCCAGAAATCTATC 3540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3774 AAATTTTTGAGTTTTATGAATCTCACTTGTGCTGTTGGAACAACTGGCCAGAAATCTATC 3833

Qy       3541 TCTAGAGTGATTGAATATTTGGAACATTGC 3570
              |||||||||||||||||||||||||||||
Db       3834 TCTAGAGTGATTGAATATTTGGAACATTGC 3863
```